Chapter 4: 4.3, 4.7, 4.13, 4.18, 4.22

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4.3

```
library(readxl)
cloth <- read_excel("cloth.xlsx")</pre>
clothLong=reshape(cloth,
                     varying = c("Bolt1", "Bolt2", "Bolt3",
                                "Bolt4", "Bolt5"),
                     v.names = "Yield", timevar = "Bolt",
                     direction = "long")
cloth.aov=aov(Yield ~ factor(Bolt) + factor(Chemical), data = clothLong)
summary(cloth.aov)
                    Df Sum Sq Mean Sq F value
                                                Pr(>F)
                     4 157.00 39.25 21.606 2.06e-05 ***
## factor(Bolt)
## factor(Chemical) 3 12.95
                                 4.32
                                        2.376
                                                 0.121
## Residuals
                   12 21.80
                                 1.82
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
MSe=summary(cloth.aov)[[1]][3,3]
H_0: T_1 = \dots = T = p = 0
```

 $H_1: T_i \neq 0$ at least one.

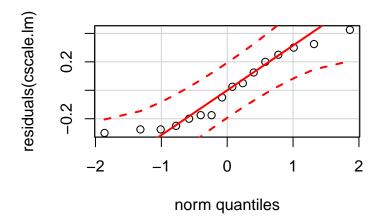
From our ANOVA we see that our chemical has an f-value of 2.376 with a p-value = 0.121. Our p-value is too big so we must fail to reject our null hypothesis and conclude that there is no differences between the treatment/chemical types.

4.7

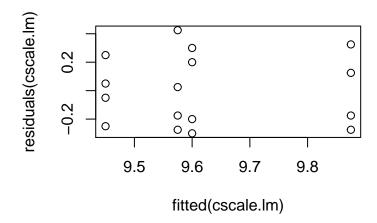
(a)

```
cscale.aov=aov(Yield ~ factor(Coupon) + factor(Tip), data = cscaleLong)
summary(cscale.aov)
                  Df Sum Sq Mean Sq F value
##
                                               Pr(>F)
## factor(Coupon) 3 0.825 0.27500 30.94 4.52e-05 ***
## factor(Tip)
                   3 0.385 0.12833
                                       14.44 0.000871 ***
## Residuals
                   9 0.080 0.00889
## ---
## Signif. codes: 0 '***' 0.001 '**' 0.05 '.' 0.1 ' ' 1
MSe=summary(cscale.aov)[[1]][3,3]
H_0: T_1 = ... = T = p = 0
_{
m VS}
H_1: T_i \neq 0 at least one.
Based on our ANOVA we see that we have a f-value of 14.44 and a p-value of 0.000871. Our p-value is
very small compare to the significance value so we must reject our null hypothesis and conclude that the
treatment/tips are significantly different.
ybar.trt=as.vector(with(cscaleLong, tapply(Yield,Tip,function(x) mean(x)))) #bar(Y_i.) vector
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[2])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.7163449
#1-3
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[3])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.09354966
#1-4
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[1]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.001488949
#2-3
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[2]-ybar.trt[3])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.05100326
#2-4
a=4;b=4;N=a*b;alpha=0.05
```

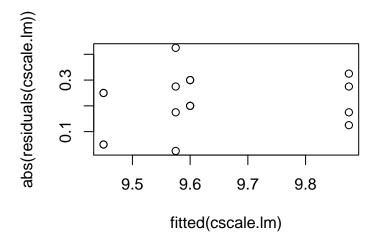
```
t0=(ybar.trt[2]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.002578639
#3-4
a=4;b=4;N=a*b;alpha=0.05
t0=(ybar.trt[3]-ybar.trt[4])/sqrt(2*MSe/b)
cri=qt(alpha/2,(a-1)*(b-1),lower.tail=F)
pvalue=2*pt(abs(t0),(a-1)*(b-1),lower.tail=F); pvalue
## [1] 0.0001290132
While using Fisher LSD we output a pvalue for the comparisons of \mu_1 = \mu_2, \mu_1 = \mu_3, \mu_1 = \mu_4, \mu_2 = \mu_3,
\mu_2 = \mu_4, and \mu_3 = \mu_4 and the results are presented above respectively. We see that the comparisons of
\mu_1 = \mu_4, \mu_2 = \mu_4, and \mu_3 = \mu_4 are different in tips of mean hardness.
 (c)
cscale.lm=lm(Yield ~ factor(Tip), data = cscaleLong)
summary(cscale.lm)
##
## Call:
## lm(formula = Yield ~ factor(Tip), data = cscaleLong)
##
## Residuals:
##
       Min
                1Q Median
                                 3Q
                                         Max
## -0.3000 -0.2125 -0.0125 0.2125 0.4250
##
## Coefficients:
##
                Estimate Std. Error t value Pr(>|t|)
## (Intercept)
                  9.5750 0.1373 69.732
                                                <2e-16 ***
## factor(Tip)2 0.0250
                              0.1942 0.129
                                                 0.900
## factor(Tip)3 -0.1250
                              0.1942 -0.644
                                                 0.532
                                                 0.148
## factor(Tip)4
                  0.3000
                              0.1942 1.545
## Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
## Residual standard error: 0.2746 on 12 degrees of freedom
## Multiple R-squared: 0.2984, Adjusted R-squared: 0.1231
## F-statistic: 1.702 on 3 and 12 DF, p-value: 0.2196
library(car)
qqPlot(residuals(cscale.lm))
```



plot(fitted(cscale.lm), residuals(cscale.lm))



plot(fitted(cscale.lm), abs(residuals(cscale.lm)))



After observing the qqplot and residual plot we see that normality is fine and there is no pattern but a structureless image on our plot. We can conclude our model is good.